



wwPDB X-ray Structure Validation Summary Report

Feb 26, 2014 – 02:23 PM GMT

PDB ID : 1VYT
Title : BETA3 SUBUNIT COMPLEXED WITH AID
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Deposited on : 2004-05-07
Resolution : 2.60 Å(reported)

This is a wwPDB validation summary report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

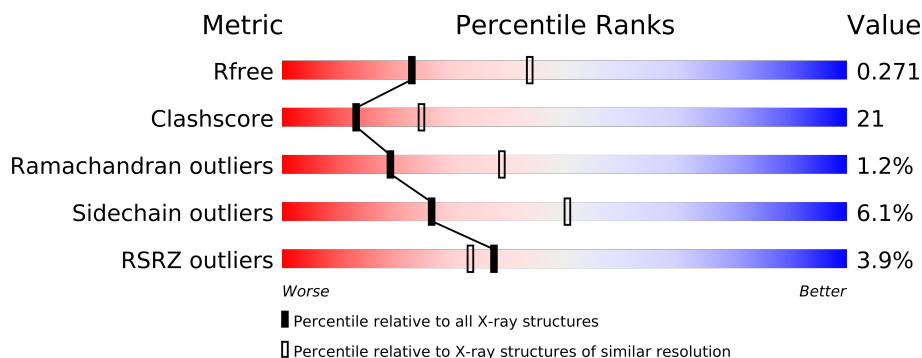
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.60 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	66092	1718 (2.60-2.60)
Clashscore	79885	2154 (2.60-2.60)
Ramachandran outliers	78287	2113 (2.60-2.60)
Sidechain outliers	78261	2113 (2.60-2.60)
RSRZ outliers	66119	1718 (2.60-2.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	351	
1	B	351	
2	E	25	
2	F	25	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4962 atoms, of which 0 are hydrogen and 0 are deuterium.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called CALCIUM CHANNEL BETA-3 SUBUNIT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	274	Total	C	N	O	S	0	0	1
			2184	1386	384	404	10			
1	B	295	Total	C	N	O	S	0	0	1
			2348	1484	420	434	10			

- Molecule 2 is a protein called VOLTAGE-DEPENDENT L-TYPE CALCIUM CHANNEL ALPHA-1C SUBUNIT.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	E	25	Total	C	N	O	0	0	0
			217	135	36	46			
2	F	17	Total	C	N	O	0	0	1
			136	87	20	29			

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	45	Total	O	0	0
			45	45		
3	B	26	Total	O	0	0
			26	26		
3	E	6	Total	O	0	0
			6	6		



● Molecule 2: VOLTAGE-DEPENDENT L-TYPE CALCIUM CHANNEL ALPHA-1C SUB-UNIT



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	252.30Å 69.00Å 60.70Å 90.00° 96.70° 90.00°	Depositor
Resolution (Å)	30.00 – 2.60 29.51 – 2.61	Depositor EDS
% Data completeness (in resolution range)	96.0 (30.00-2.60) 95.9 (29.51-2.61)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.27 (at 2.61Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.231 , 0.272 0.231 , 0.271	Depositor DCC
R_{free} test set	3065 reflections (11.16%)	DCC
Wilson B-factor (Å ²)	45.8	Xtriage
Anisotropy	0.394	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 30.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 31519 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	4962	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.37% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.44	0/2226	0.65	0/3009
1	B	0.38	0/2393	0.64	2/3234 (0.1%)
2	E	0.43	0/219	0.54	0/291
2	F	0.51	0/138	0.81	0/187
All	All	0.42	0/4976	0.64	2/6721 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	295	SER	N-CA-C	5.63	126.21	111.00
1	B	294	VAL	N-CA-C	-5.05	97.37	111.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2184	0	2204	80	0
1	B	2348	0	2379	108	0
2	E	217	0	208	6	0
2	F	136	0	124	14	0
3	A	45	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	26	0	0	0	0
3	E	6	0	0	0	0
All	All	4962	0	4915	202	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 21.

The worst 5 of 202 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:205:LYS:HE2	1:B:214:ILE:HG13	1.37	1.04
1:B:182:LEU:HD23	1:B:290:VAL:HB	1.36	1.02
1:A:275:ASN:H	1:A:279:GLN:HE22	1.03	1.01
1:B:56:LYS:HG3	1:B:115:ILE:HG13	1.40	0.99
1:B:230:ASN:HB3	1:B:232:PRO:HD2	1.45	0.98

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	268/351 (76%)	255 (95%)	13 (5%)	0	100	100
1	B	291/351 (83%)	265 (91%)	20 (7%)	6 (2%)	11	19
2	E	23/25 (92%)	21 (91%)	2 (9%)	0	100	100
2	F	15/25 (60%)	12 (80%)	2 (13%)	1 (7%)	2	2
All	All	597/752 (79%)	553 (93%)	37 (6%)	7 (1%)	19	39

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	362	HIS
1	B	184	GLY
1	B	332	SER

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Mol	Chain	Res	Type
1	B	130	LYS
1	B	191	GLU

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	242/310 (78%)	237 (98%)	5 (2%)	66	90
1	B	261/310 (84%)	242 (93%)	19 (7%)	20	38
2	E	23/23 (100%)	18 (78%)	5 (22%)	1	2
2	F	14/23 (61%)	10 (71%)	4 (29%)	0	1
All	All	540/666 (81%)	507 (94%)	33 (6%)	26	50

5 of 33 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	228	VAL
1	B	245	SER
2	F	438	LEU
1	B	240	ARG
1	B	241	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	50	GLN
1	B	51	GLN
1	B	265	GLN
1	A	361	HIS
1	B	311	GLN

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	274/351 (78%)	-0.12	8 (2%) 49 46	20, 38, 89, 122	0
1	B	295/351 (84%)	0.03	12 (4%) 35 32	32, 55, 90, 119	0
2	E	25/25 (100%)	-0.06	0 100 100	21, 40, 76, 84	0
2	F	17/25 (68%)	1.02	4 (23%) 1 1	57, 82, 121, 121	0
All	All	611/752 (81%)	-0.01	24 (3%) 37 33	20, 47, 90, 122	0

The worst 5 of 24 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	133	GLN	4.6
1	B	135	ALA	3.9
1	A	43	GLU	3.7
1	B	167	HIS	3.4
1	B	363	PRO	3.4

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.